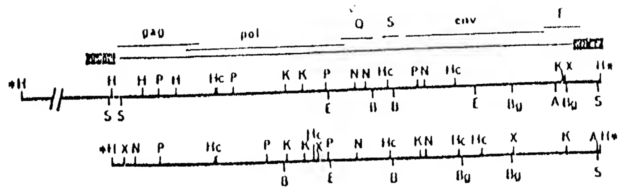

gag
pol
Q
S
env
F
LAV eli
LAV mal

FIG. 1A

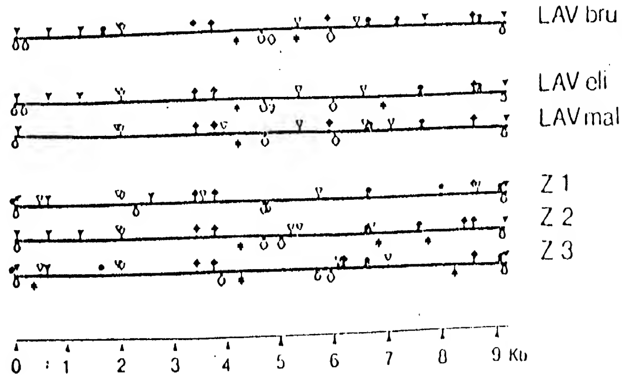
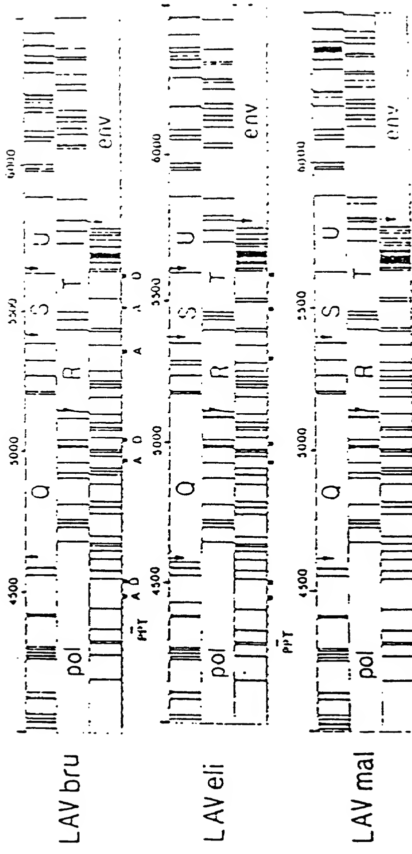

LAV bru
LAV eli
LAV mal
Z 1
Z 2
Z 3
0
1
2
3
4
5
6
7
8
9 Kb

FIG. 1B

FIG. 2



Coll
GG

GAG

```
                                                                              p25
                    10         20         30         40         50         60         70         80
LAV BRU     MGARASVLSG GELDRWEKIR LRPGGKKKYK LKHIVWASRE LERFAVNPGL LETSEGCRQI LGQLQPSLQT GSEELRSLYN
ARV 2                      K
LAV HAL                 K  A               R    L            L        G   Q   HE   ST K      IK
LAV ELI                 K  K               R               Y L            K   I     AI    T

                    90        100        110        120        130        140        150        160
LAV BRU     TVATLYCVHQ RIEIKDTKEA LDKIEEEQNK SKKKAQQAAA ------DTGN SSQVSQNYPI VQNIQGQMVH QAISPRTLNA
ARV 2                    DV        E                    ----AAC  N               L
LAV HAL                  DV             I     RQ T      AQQAAAA KN   S           A    I
LAV ELI              K G DV        E N                  ------   N N             L

                   170        180        190        200        210        220        230        240
LAV BRU     WVKVVEEKAF SPEVIPMFSA LSEGATPQDL NTMLNTVGGH QAAMQMLKET INEEAAEWDR VHPVHAGPIA PGQMREPRGS
ARV 2
LAV HAL         I                             N   I             D        D             P
LAV ELI         I                                                                 L

                   250        260        270        280        290        300        310        320
LAV BRU     DIAGTTSTLQ EQIGWMTNNP PIPVGEIYKR WIILGLNKIV RMYSPTSILD IRQGPKEPFR DYVDRFYKTL RAEQASQEVK
ARV 2                                                                                           D
LAV HAL                       S        D                     V                      F         T
LAV ELI                   A   S                 V            V                                  D

                                                                                     p13
                   330        340        350        360        370        380        390        400
LAV BRU     NWMTETLLVQ NANPDCKTIL KALGPAATLE EMMTACQGVG GPGHKARVLA EAMSQVTNS- ATIMMQRGNF RNQRKIVKCF
ARV 2                                                                          P-  N              T
LAV HAL                                G                  S            A   T  A         KG - KI
LAV ELI                                Q                  S            A   V T A        KGP  I

                   410        420        430        440        450        460        470        480
LAV BRU     NCGKEGHIAR NCRAPRKKGC WKCGKEGHQM KDCTERQANF LGKIWPSYKG RPGNFLQSRP EPTAPPFLQS RPEPTAPPLE
ARV 2                K             R  R                                             ---- --------
LAV HAL            L                                           N                    ---- --------A
LAV ELI              K             R       L              K    N                    ---- --------A

                   490        500        510
LAV BRU     SFRSGVETTT PSQKQEPIDK ELYPLTSLRS LFGNDPSSQ
ARV 2          F E K
LAV HAL       GF E IK-      QK         A  K      QL
LAV ELI       GF E I -      QK            K        L
```

FIG. 3A

Central region : Q

```
                  10         20         30         40         50         60         70         80
LAV BRU   HENRWQVHIV WQVDRHRIRT WKSLVKHHHY VSCKARCWFY KHHYESPHPR ISSEVHIPLC DARLVITTYW GLHTCERDWH
ARV 2                                      I K  K           T    V            K               E
LAV HAL                          H           K  KH          R  K V               VH      Q   K
LAV ELI                      K               K  HR             K            E     K           E

                  90        100        110        120        130        140        150        160
LAV BRU   LGQGVSIEWR KKRYSTQVDP ELADQLIHLY YFDCFSDSAI RKALLGHIVS PRCEYQAGHH KVGSLQYLAL AALITPKKIK
ARV 2          A       K        G        H       E    KH I  YR                                 T
LAV HAL     H        Q      L   D                E     Q I          D                   T   A  TR
LAV ELI               R         G       H        E       I  D                           T   A  Q

                 170        180        190
LAV BRU   PPLPSVTKLT EDRWNKPQKT KGHRGSHTHN GH
ARV 2           K
LAV HAL         R            Q
LAV ELI         R            Q  R
```

R

```
                  10         20         30         40         50         60         70         80
LAV BRU   HEQAPEDQGP QREPHHEWTL ELLEELKNEA VRHFPRIWLH GLGQHIYETY GDTWAGVEAI IRILQQLLFI HFRIGCRHSR
ARV 2                    Y             R         P    S   Y                                  Q
LAV HAL        A                       Q              S              E        S              Q
LAV ELI        A         Y   A         S              S              V                       Q

                  90
LAV BRU   IGVTQQRRAR -NGASRS
ARV 2       II       R
LAV HAL     I R      -  S
LAV ELI     IIR      -  S
```

S (tat)

```
                  10         20         30         40         50         60         70
LAV BRU   HEPVDPRLEP WKHPGSQPKT ACTTCYCKKC CFHCQVCFTT KALGISYGRK KRRQRRRPPQ GSQTHQVSLS KQ
ARV 2           N            R    HH           YA   R  G                A   D     A
LAV HAL    D    N     N      R  P HK        Y   H  I   G                     H A  DP P L
LAV ELI    D    N     N      R  P HK H      Y  P   LH  G               C     C A  PIP
```

FIG. 3B

POL

```
                 10         20         30         40         50         60         70         80
LAV BRU  FPREDLAFLQ GKAREFSSEQ TRANSPTFSS EQTRANSPTR RELQVWGRDN NSLSEAGADR QCTVSFNFPQ ITLWQRPLVT
ARV 2                                 --- ---------        GE
LAV HAL      H   P        P           --- ---------S    R   G - KT   T  E    I  S            V
LAV ELI      H   P     G L PK         --- ---------S    R     -  P KT   E                      A

                 90        100        110        120        130        140        150        160
LAV BRU  IKIGGQLKEA LLDTGADDTV LEEMSLPGRW KPKMIGGIGG FIKVRQYDQI LIEICGHKAI GTVLVGPTPV NIIGRNLLTQ
ARV 2     R                        N   K                        PV
LAV HAL  VRV                      IN   K                              K      I             H
LAV ELI                            N   K                        P     Q

                170        180        190        200        210        220        230        240
LAV BRU  IGCTLNFPIS PIETVPVKLK PGMDGPKVKQ WPLTEEKIKA LVEICTEMEK EGKISKIGPE NPYNTPVFAI KKKDSTKWRK
ARV 2
LAV HAL                              R                T   KD        L
LAV ELI                                               T    D         R          I

                250        260        270        280        290        300        310        320
LAV BRU  LVDFRELNKR TQDFWEVQLG IPHPAGLKKK KSVTVLDVGD AYFSVPLDED FRKYTAFTIP SINNETPGIR YQYNVLPQGW
ARV 2                                                       K
LAV HAL    N
LAV ELI                                                                 S

                330        340        350        360        370        380        390        400
LAV BRU  KGSPAIFQSS MTKILEPFRK QNPDIVIYQY MDDLYVGSDL EIGQHRTKIE ELRQHLLRWG LTTPDKKHQK EPPFLWMGYE
ARV 2                                                                      F
LAV HAL                      T K  E                                E   K    F
LAV ELI                           EN                           K  E        F R

                410        420        430        440        450        460        470        480
LAV BRU  LNPDKWTVQP IVLPEKDSWT VNDIQKLVGK LNWASQIYPG IKVRQLCKLL RGTKALTEVI PLTEEAELEL AENREILKEP
ARV 2                H                           A     K
LAV HAL              Q  D E                            K         A    DIV    A
LAV ELI           S  K    E         N  ER

                490        500        510        520        530        540        550        560
LAV BRU  VHGVYYDPSK DLIAEIQKQG QGQWTYQIYQ EPFKNLKTGK YARTRGAHTN DVKQLTEAVQ KITTESIVIW GKTPKFKLPI
ARV 2      E          V                                H                   VS          I
LAV HAL                                   QY           IKS                  AQ            K
LAV ELI                        H                       H            A     K S         K    R
```

FIG. 3C

FIG. 3D

```
                   570        580        590        600        610        620        630        640
LAV BRU     QKETWETWWT EYWQATWIPE WEFVNTPPLV KLWYQLEKEP IVGAETFYVD GAASRETKLG KAGYVTNRGR QKVVTLTDTT
ARV 2             A  N                                                N             D        SIA
LAV HAL           A                                 T                 N    K        D        S  E
LAV ELI              A                                   I            N             D        P

                   650        660        670        680        690        700        710        720
LAV BRU     NQKTELQAIH LALQDSGLEV NIVTDSQYAL GIIQAQPDKS ESELVNQIIE QLIKKEKVYL AWVPAHKGIG GNEQVDKLVS
ARV 2                                                    S
LAV HAL                       S                            I          Q D     S
LAV ELI              N

                   730        740        750        760        770        780        790        800
LAV BRU     AGIRKVLFLD GIDKAQDEHE KYHSNWRAMA SDFNLPPVVA KEIVASCDKC QLKGEAMHGQ VDCSPGIWQL DCTHLEGKVI
ARV 2                N       E                                                                  I
LAV HAL     S                E                      I                                           I
LAV ELI     Q                E       N

                   810        820        830        840        850        860        870        880
LAV BRU     LVAVHVASGY IEAEVIPAET GQETAYFLLK LACRWPVKTI HTDNGSNFTS TTVKAACWWA GIKQEFGIPY NPQSQGVVES
ARV 2
LAV HAL     I                            I           VV            AA         N
LAV ELI                                              VV            AA

                   890        900        910        920        930        940        950        960
LAV BRU     MHKELKKIIG QVRDQAEHLK TAVQMAVFIH NFKRKGGIGG YSAGERIVDI IATDIQTKEL QKQITKIQNF RVYYRDSRDP
ARV 2         N                                                                                NK
LAV HAL               E                                    I N                                 N
LAV ELI                                      NR            I                  I

                   970        980        990       1000       1010
LAV BRU     LWKGPAKLLW KGEGAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAS RQDED
ARV 2
LAV HAL     I                                                    G C
LAV ELI     I                     K           V
```

ENV

```
                                SP      |                        OMP
                10         20         30 ●|       40         50         ● 60         70        ● 80
LAV BRU   MRVK---EKY QNLWRWGWKW GTMLLGILMI CSATEKLWVT VYYGVPVWKE ATTTLFCASD AKAYDTEVHN VWATHACVPT
ARV 2      K  GTRRN            --- - L   H                                    K
LAV HAL      REIQRN   NW       --- -H    H  T   IA D                           S E        I
LAV ELI     ARGIENR[C] NW K    --- -I       T     ADN                          S E  A     I

                90        100        110        120 ●     1|30  ● 140        150        160
LAV BRU   DPNPQEVVLV NVTENFNMWK NDMVEQMHED IISLWDQSLK PCVKLTPLCV SLKCTDL-GN ATNTNSSNTN SSSGEMMME-
ARV 2              C .        N     Q                        T N    - K         --- ----GUKE I
LAV HAL         IE E     C    N                               T N  NVN T  V GTNAGS  NTNA LK  I
LAV ELI         IA E          N                               T N S E--L RN GTNG NV TTLEKG----

              ●170        180        190        200        210 ●     22|0       230  ●     240
LAV BRU   KGEIKNCSFN ISTSIRGKVQ KEYAFFYKLD IIPIDNDTTS -----YTLTS CNTSVITQAC PKVSFEPIPI HYCAPAGFAI
ARV 2                T   D I    N L RN   VV    AS T THYTH K IN   K                     T
LAV HAL   -  V       TPVGSD R  -   T  N  LVQ  DSDN ----S K IN                T D
LAV ELI   ---N       VT VLKD K QV  L  K    V    SST -NSTN K IN     A

          ●     250 ●     260 ●      270        280        290        300        310 ●      320
LAV BRU   LKCNNKTFNG TGPCTNVSTV QCTHGIRPVV STQLLLNGSL AEEEVVIRSA NFTDNAKTII VQLNQSVEIN CTRPNNNTRK
ARV 2                K                I                       D    N            L  A
LAV HAL       D K      EI K           K                  IN   E   L   T N      ET T      G    K
LAV ELI      RD K                                         I   E   L N   N    AN  E  K T  A  YQ   Q

                330        340       ●350        360        370        380        390   ●   400
LAV BRU   SIRIQRGPGR AFVTIGK-IG NMRQAHCNIS RAKWNATLKQ IASKLREQFG NNKT-IIFKQ SSGGDPEIVT HSFNCGGEFF
ARV 2       Y --        N T RI  DI K         Q  N  E   VK          - V N            H     K
LAV HAL   C NF--    Q   LY T I-V DI K Y T N ETE DK  Q  V V  GSLL- -   K   NS          T     R
LAV ELI   RTP -- L Q SLY TKS-RS IIG          Q SK  Q  V R  GTLL- -   I K  P          T

          ●     410        420        430  ●     440        450        460  ●     470        480
LAV BRU   YCNSTQLFNS TWFNSTWSTE GSNNTEGSDT ITLPCRIKQF INMWQEVGKA MYAPPISGQI RCSSNITGLL LTRDGGNN--
ARV 2        T    N  -----RLN NTEG K N    I       I                   G    S                  T -V
LAV HAL      TSK      Q NGARL- -  S  STGS          I      KT         A V  N L      I        NSSD
LAV ELI      TSG      NI A NHI TES NSTNTN    Q     I   K VAGR-  I      ERN   L                 I --

                                                           |   TMP
                490        500        510        520        530|      540        550        560
LAV BRU   NNGSEIFRPG GGDMRDNWRS ELYKYKVVKI EPLGVAPTKA KRRVVQREKR AVGI-GALFL GFLGAAGSTM GARSMTLTVQ
ARV 2     T DT V                          I        I                  V  N             V L
LAV HAL     SDN TL               I         R                   E     I L-  N             A L
LAV ELI     STN T                          Q          K        E     I I-  N               V
```

FIG. 3E

```
                   570        580        590        600        610        620        630        640
LAV BRU     ARQLLSGIVQ QQNHLLRAIE AQQHLLQLTV WGIKQLQARI LAVERYLKDQ QLLGIWGCSG KLICTTAVPW HASWSNKSLE
ARV 2                                                 V        R
LAV HAL                                               V        Q   R   H       H    P     S    K  D
LAV ELI         H                                                              H    H     S    K  N

                   650        660        670        680        690        700        710        720
LAV BRU     QIWHHNTWHE WDREIHNYTS LIHSLIEESQ NQQEKNEQEL LELDKWASLW NWFNITNWLW YIKIFIMIVG GLVGLRIVFA
ARV 2       D  D     Q  E   D   K T YT L                              S
LAV HAL     C        Q  EK  S   G I YN       I      K                 S SK      R   IV     I    I
LAV ELI     E  Q        E   D   G   Y        T      K                 S  Q            I    I

                   730        740        750        760        770        780        790        800
LAV BRU     VLSIVNRVRQ GYSPLSFQTH LPTPRGP-DR PLGIEEEGGE RDRDRSIRLV NGSLALIWDD LRSLCLFSYH RLRDLLLIVT
ARV 2                           R   V    -    D               V    D F     E           K         AA
LAV HAL        L             L  L        P              QG G         IS         H                A
LAV ELI        L                L   A    -      T        G    V  L   IS                       I  AV

                   810        820        830        840        850        860        870
LAV BRU     RIVELLGRRG WEALKYWWNL LQYWSQELKN SAVSLLNATA IAVAEGTDRV IEVVQGACRA IRHIPRRIRQ GLERILL
ARV 2         T I  H           S      I          W         T          A R Y    L  H          L
LAV HAL                      L        G        I    T        C       IG RYG    L          F  A
LAV ELI                 DI   L            R    S  FD I               II R     VLN            S

F
                    10         20         30         40         50         60         70         80
LAV BRU    .MGGKWSKSSV VGWPTVRERM R----RAEPA ADGVGAASR- ----DLEKHG AITSSNTAAT NAACAWLEAQ EE-LEVGFPV
ARV 2              K N G  SAI      RAEP            V  - ----                    D          -
LAV HAL              I     KI   I  ---- TP T LT    V QD AVSQ  D C   AA   SP  N   S --- PP   E
LAV ELI              I     AI   I  ---- TN         V  - ----               S    D          SD

                    90        100        110        120        130        140        150        160
LAV BRU     TPQVPLRPMT YKAAVDLSHF LKEKGGLEGL IHSQRRQDIL DLWIYHTQGY FPDWQNYTPG PGVRYPLTFG WCYKLVPVEP
ARV 2       K              L I                W     E                           I          F
LAV HAL     K            G F             D   VG PK  E      V                    I F        I    HS
LAV ELI     K            E L                  W KK  E      V H   I              I           E    D

                   170        180        190        200        210
LAV BRU     DKVEEANKGE NTSLLHPVSL HGMDDPEREV LEWRFDSRLA FHHVARELHP EYFKNC
ARV 2       E      E   H      H      E A K    V     K      H         Y D
LAV HAL     EE     E    HC    I Q    E A      K K   S   LR R   Q     Y D
LAV ELI     QE   DTE   TN     ICQ    E    Q   K   H      E K   H    FY  -
```

FIG. 3F

FIG. 4A

A

LAVbru vs.	GAG		POL		ENV Total		ENV OMP		ENV TMP	
HTLV-3 USA	512 0/0	0.8	1015 0/0	1.3	856 5/0	1.4	507 5/0	1.6	349 0/0	1.1
ARV-2 USA	502 12/2	3.4	1003 12/0	3.1	855 17/11	13.0	505 17/10	14.3	350 0/1	11.2
LAVeli Zaire	500 13/1	9.8	1002 13/0	5.5	853 22/14	20.7	504 22/14	25.3	349 0/0	13.8
LAVmal Zaire	505 14/7	12.0	1002 13/0	7.7	859 13/11	21.7	509 13/10	26.4	350 0/1	14.9

B

LAVeli vs.	GAG		POL		ENV Total		ENV OMP		ENV TMP	
LAVmal	505 1/6	10.8	1002 0/0	8.4	859 13/11	19.8	509 8/13	23.6	350 0/1	14.3

FIG. 4B

A

LAVbru vs.	orf F		central region: orf Q		orf R		orf S	
HTLV-3 USA	206 0/0	1.5	192 0/0	0	,	nd	80 0/0	2.5
ARV-2 USA	210 0/4	12.6	192 0/0	10.0	97 0/1	9.4	81 0/1	15.0
LAVeli Zaire	206 1/1	19.4	192 0/0	10.4	96 0/0	11.5	80 0/0	27.5
LAVmal Zaire	209 2/5	27.0	192 0/0	12.6	96 0/0	10.4	80 0/0	23.8

B

LAVeli vs.	orf F		orf Q		orf R		orf S	
LAVmal	209 3/6	22.5	192 0/0	12.0	96 0/0	6.3	80 0/0	11.3

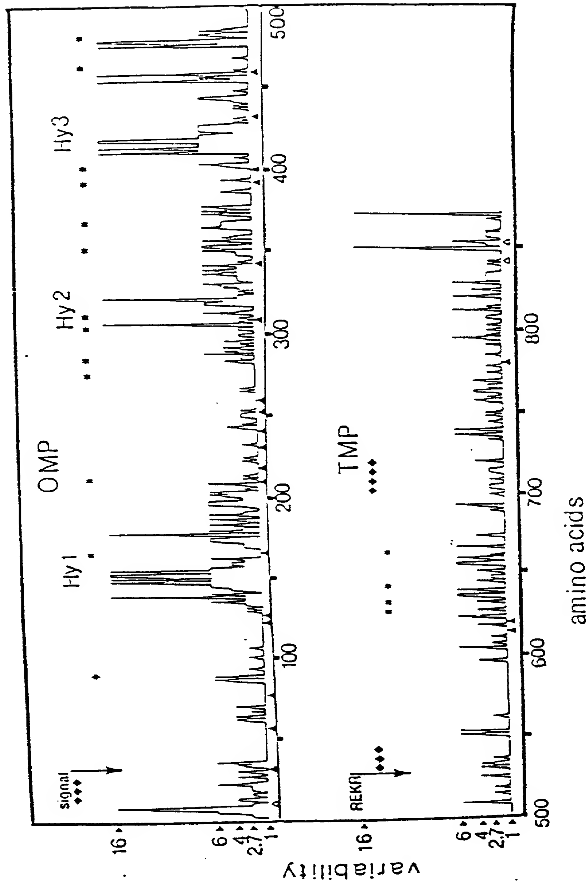


FIG. 5

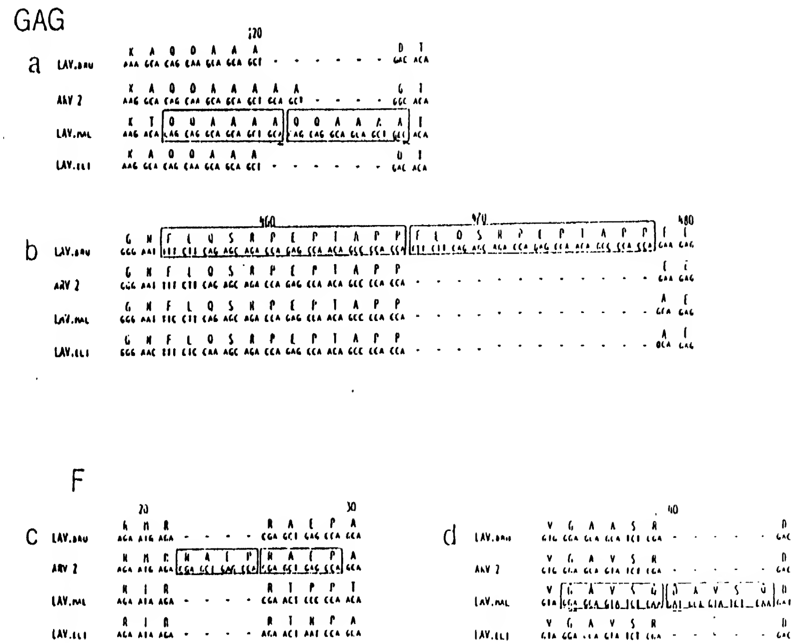


FIG. 6A

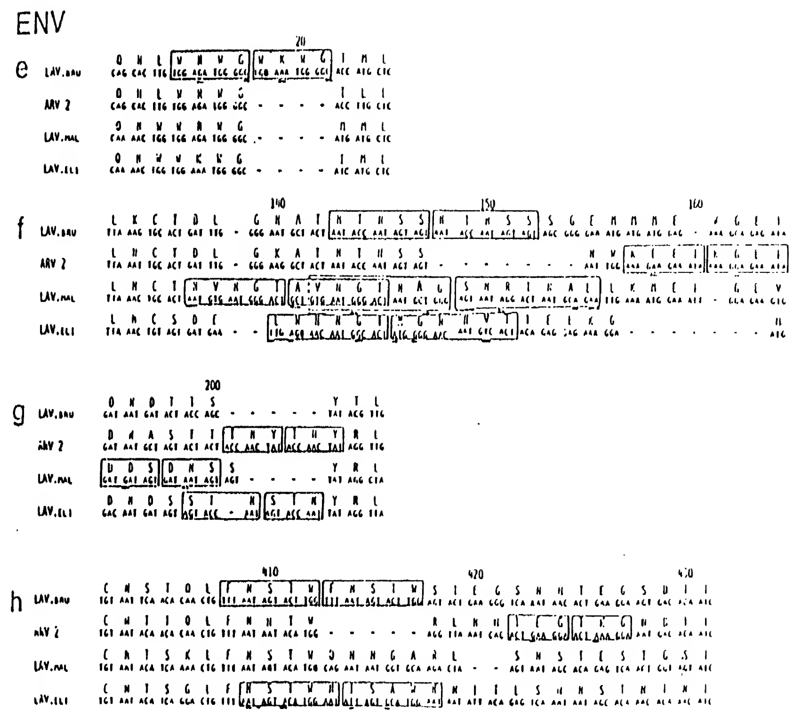


FIG. 6B

FIG. 7A

LAV.ELI

R

GGTCTCTCTGGTTAGACCAGATTTGAGCCTGGGAGCTCTCTGGCTAGCTAGGGAACCCAC

R ←→ U5

TGCTTAAGCCTCAATAAAGCTTGCCTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGT

100

GTGACTCTGGTAACTAGAGATCCCTCAGACCCCTTTAGTCAGAGTGGAAAATCTCTAGCA

U5←

GTGGCGCCCGAACAGGGACCTGAAAGCGAAAGTAGAACCAGAGGAGCTCTCTCGACGCAG

200

GACTCGGCTTGCTGAAGCGCGCACGGCAAGAGGCGAGGGGCAGCGACTGGTGAGTACGCT

→GAG 300

MetGlyAlaArgAlaSerValLeuSer
AAAATTTTGACTAGCGGAGGCTAGAAGGAGAGAGATGGGTGCGAGAGCGTCAGTATTAA

GlyGlyLysLeuAspLysTrpGluLysIleArgLeuArgProGlyGlyLysLysLysTyr
GCGGGGGAAAATTAGATAAATGGGAAAAAATTCGGTTACGGCCAGGAGGAAAGAAAAAAT

400

ArgLeuLysHisIleValTrpAlaSerArgGluLeuGluArgTyrAlaLeuAsnProGly
ATAGACTAAAACATATAGTATGGGCAAGCAGGGAGCTAGAACGATATGCACTTAATCCTG

LeuLeuGluThrSerGluGlyCysLysGlnIleIleGlyGlnLeuGlnProAlaIleGln
GCCTTTTAGAAACATCAGAAGGCTGTAAACAAATAATAGGGCAGCTACAACCAGCTATTC

500

ThrGlyThrGluGluLeuArgSerLeuTyrAsnThrValAlaThrLeuTyrCysValHis
AGACAGGAACAGAAGAACTTAGATCATTATATAATACAGTAGCAACCCTCTATTGTGTAC

600

LysGlyIleAspValLysAspThrLysGluAlaLeuGluLysMetGluGluGluGlnAsn
ATAAAGGAATAGATGTAAAAGACACCAAGGAAGCTTTAGAAAAGATGGAGGAAGAGCAAA

LysSerLysLysLysAlaGlnGlnAlaAlaAlaAspThrGlyAsnAsnSerGlnValSer
ACAAAAGTAAGAAAAAAGGCACAGCAAGCAGCAGCTGACACAGGAAACAACAGCCAGGTCA

700

GlnAsnTyrProIleValGlnAsnLeuGlnGlyGlnMetValHisGlnAlaIleSerPro
GCCAAAATTATCCTATAGTGCAGAACCTACAGGGGCAAATGGTACATCAGGCCATATCAC

ArgThrLeuAsnAlaTrpValLysValIleGluGluLysAlaPheSerProGluValIle
CTAGAACTTTGAACGCATGGGTAAAAGTAATAGAAGAAAAGGCTTTCAGCCCAGAAGTAA

800

ProMetPheSerAlaLeuSerGluGlyAlaThrProGlnAspLeuAsnThrMetLeuAsn
TACCCATGTTTTCAGCATTATCAGAAGGAGCCACCCCACAAGATTTAAACACCATGCTAA

900

ThrValGlyGlyHisGlnAlaAlaMetGlnMetLeuLysGluThrIleAsnGluGluAla
ACACAGTGGGGGGACATCAAGCAGCCATGCAAATGCTAAAAGAGACCATCAATGAAGAAG

AlaGluTrpAspArgLeuHisProValHisAlaGlyProIleAlaProGlyGlnMetArg
CTGCAGAATGGGATAGGTTACATCCAGTGCATGCAGGGCCTATTGCACCAGGCCAGATGA

1000

GluProArgGlySerAspIleAlaGlyThrThrSerThrLeuGlnGluGlnIleAlaTrp
GAGAACCAAGGGGAAGTGATATAGCAGGAACTACTAGTACCCTTCAGGAACAAATAGCAT

MetThrSerAsnProProIleProValGlyGluIleTyrLysArgTrpIleIleValGly
GGATGACAAGTAACCCACCTATCCCAGTAGGAGAAATCTATAAAAGATGGATAATTGTGG

1100

LeuAsnLysIleValArgMetTyrSerProValSerIleLeuAspIleArgGlnGlyPro
GATTAAATAAAATAGTAAGAATGTATAGCCCTGTCAGCATTTTGGACATAAGACAGGGAC

1200

FIG. 7B

LysGluProPheArgAspTyrValAspArgPheTyrLysThrLeuArgAlaGluGlnAla
CAAAGGAACCTTTTAGAGACTATGTAGACCGGTTCTATAAAACTCTAAGAGCCGAGCAAG

SerGlnAspValLysAsnTrpMetThrGluThrLeuLeuValGlnAsnAlaAsnProAsp
CTTCACAGGATGTAAAAAATTGGATGACAGAAACCTTGTTGGTCCAAAATGCAAACCCAG
1300

CysLysThrIleLeuLysAlaLeuGlyProGlnAlaThrLeuGluGluMetMetThrAla
ATTGCAAGACTATCTTAAAAGCATTGGGACCACAGGCTACACTAGAAGAAATGATGACAG

CysGlnGlyValGlyGlyProSerHisLysAlaArgValLeuAlaGluAlaMetSerGln
CATGTCAGGGAGTGGGGGGCCCAGCCATAAAGCAAGAGTTCTGGCTGAGGCAATGAGCC
1400

AlaThrAsnSerValThrThrAlaMetMetGlnArgGlyAsnPheLysGlyProArgLys
AAGCAACAAATTCAGTTACTACAGCAATGATGCAGAGAGGCAATTTTAAGGGCCCAAGAA
1500

IleIleLysCysPheAsnCysGlyLysGluGlyHisIleAlaLysAsnCysArgAlaPro
AAATTATTAAGTGTTTCAATTGTGGCAAAGAAGGGCACATAGCAAAAAATTGCAGGGCCC

ArgLysLysGlyCysTrpArgCysGlyLysGluGlyHisGlnLeuLysAspCysThrGlu
CTAGGAAAAAGGGCTGTTGGAGATGTGGAAAGGAAGGACACCAACTAAAAGATTGCACTG
1600

→POL
PhePheArgGluAsnLeuAlaPheProGlnGlyLysAlaGlyGluLeu
ArgGlnAlaAsnPheLeuGlyArgIleTrpProSerHisLysGlyArgProGlyAsnPhe
AGAGACAGGCTAATTTTTTAGGGAGAATTTGGCCTTCCCACAAGGGAAGGCCGGGGAACT

SerProLysGlnThrArgAlaAsnSerProThrSerArgGluLeuArgValTrpGlyArg
LeuGlnSerArgProGluProThrAlaProProAlaGluSerPheGlyPheGlyGluGlu
TTCTCCAAAGCAGACCAGAGCCAACAGCCCCACCAGCAGAGAGCTTCGGGTTTGGGGAAG
1700

AspAsnProLeuSerLysThrGlyAlaGluArgGlnGlyThrValSerPheAsnPhePro
IleThrProSerGlnLysGlnGluGlnLysAspLysGluLeuTyrProLeuThrSerLeu
AGATAACCCCCTCTCAAAAACAGGAGCAGAAAGACAAGGAACTGTATCCTTTAACTTCCC
1800

GAG←
GlnIleThrLeuTrpGlnArgProLeuValAlaIleLysIleGlyGlyGlnLeuLysGlu
LysSerLeuPheGlyAsnAspProLeuSerGln
TCAAATCACTCTTTGGCAACGACCCCTTGTCGCAATAAAAATAGGGGGACAGCTAAAGGA

AlaLeuLeuAspThrGlyAlaAspAspThrValLeuGluGluMetAsnLeuProGlyLys
AGCTCTATTAGATACAGGAGCAGATGATACAGTATTAGAAGAAATGAATTTGCCAGGAAA
1900

TrpLysProLysMetIleGlyGlyIleGlyGlyPheIleLysValArgGlnTyrAspGln
ATGGAAACCAAAAATGATAGGGGGAATTGGAGGTTTTATCAAAGTAAGACAGTATGATCA

IleProIleGluIleCysGlyGlnLysAlaIleGlyThrValLeuValGlyProThrPro
AATACCCATAGAAATCTGTGGACAGAAAGCTATAGGTACAGTATTAGTAGGACCTACGCC
2000

ValAsnIleIleGlyArgAsnLeuLeuThrGlnIleGlyCysThrLeuAsnPheProIle
TGTCAACATAATCGGAAGAAATTTGTTGACCCAGATTGGCTGCACTTTAAATTTTCCAAT
2100

SerProIleGluThrValProValLysLeuLysProGlyMetAspGlyProLysValLys
TAGTCCTATTGAAACTGTACCAGTAAAATTAAAGCCAGGAATGGATGGCCCAAAAGTTAA

GlnTrpProLeuThrGluGluLysIleLysAlaLeuThrGluIleCysThrAspMetGlu
ACAATGGCCATTGACAGAAGAAAAAATAAAAGCATTAACAGAAATTTGTACAGATATGGA
2200

FIG. 7C

```
 LysGluGlyLysIleSerArgIleGlyProGluAsnProTyrAsnThrProIlePheAla
AAAGGAAGGAAAAATTTCAAGAATTGGGCCTGAAAATCCATACAATACTCCAATATTTGC

 IleLysLysLysAspSerThrLysTrpArgLysLeuValAspPheArgGluLeuAsnLys
CATAAAGAAAAAAGACAGTACCAAGTGGAGAAAATTAGTAGATTTCAGAGAACTTAATAA
             2300
 ArgThrGlnAspPheTrpGluValGlnLeuGlyIleProHisProAlaGlyLeuLysLys
GAGAACTCAAGATTTCTGGGAAGTTCAATTAGGAATACCGCATCCTGCAGGGCTGAAAAA
                                                        2400
 LysLysSerValThrValLeuAspValGlyAspAlaTyrPheSerValProLeuAspGlu
GAAAAAATCAGTAACAGTACTGGATGTGGGTGATGCATATTTTTCAGTTCCCTTAGATGA

 AspPheArgLysTyrThrAlaPheThrIleSerSerIleAsnAsnGluThrProGlyIle
AGATTTTAGGAAATATACCGCCTTTACCATATCTAGTATAAACAATGAGACACCAGGGAT
                                         2500
 ArgTyrGlnTyrAsnValLeuProGlnGlyTrpLysGlySerProAlaIlePheGlnSer
TAGATATCAGTACAATGTGCTTCCACAGGGATGGAAAGGATCACCGGCAATATTCCAAAG

 SerMetThrLysIleLeuGluProPheArgLysGlnAsnProGluMetValIleTyrGln
TAGCATGACAAAAATCTTAGAGCCCTTTAGAAAACAAAATCCAGAAATGGTTATCTATCA
             2600
 TyrMetAspAspLeuTyrValGlySerAspLeuGluIleGlyGlnHisArgThrLysIle
ATACATGGATGATTTGTATGTAGGATCTGACTTAGAAATAGGGCAGCATAGGACAAAAAT
                                                        2700
 GluLysLeuArgGluHisLeuLeuArgTrpGlyPheThrArgProAspLysLysHisGln
AGAGAAATTAAGAGAACATCTATTGAGGTGGGGATTTACCAGACCAGATAAAAAACATCA

 LysGluProProPheLeuTrpMetGlyTyrGluLeuHisProAspLysTrpThrValGln
GAAAGAACCCCCATTTCTTTGGATGGGTTATGAACTCCATCCTGATAAATGGACAGTACA
                                         2800
 SerIleLysLeuProGluLysGluSerTrpThrValAsnAspIleGlnAsnLeuValGlu
GTCTATAAAACTGCCAGAAAAGGAGAGCTGGACTGTCAATGATATACAGAACTTAGTGGA

 ArgLeuAsnTrpAlaSerGlnIleTyrProGlyIleLysValArgGlnLeuCysLysLeu
GAGATTAAACTGGGCAAGCCAGATTTATCCAGGAATTAAAGTAAGACAATTATGTAAACT
             2900
 LeuArgGlyThrLysAlaLeuThrGluValIleProLeuThrGluGluAlaGluLeuGlu
CCTTAGGGGAACCAAAGCACTAACAGAAGTAATACCACTAACAGAAGAAGCAGAATTAGA
                                                        3000
 LeuAlaGluAsnArgGluIleLeuLysGluProValHisGlyValTyrTyrAspProSer
ACTGGCAGAAAACAGGGAAATTTTAAAAGAACCAGTACATGGAGTGTATTATGACCCATC

 LysAspLeuIleAlaGluIleGlnLysGlnGlyHisGlyGlnTrpThrTyrGlnIleTyr
AAAAGACTTAATAGCAGAAATACAGAAACAAGGGCACGGCCAATGGACATACCAAATTTA
                                         3100
 GlnGluProPheLysAsnLeuLysThrGlyLysTyrAlaArgMetArgGlyAlaHisThr
TCAAGAACCATTTAAAAATCTGAAAACAGGAAAGTATGCAAGAATGAGGGGTGCCCACAC

 AsnAspValLysGlnLeuAlaGluAlaValGlnArgIleSerThrGluSerIleValIle
TAATGATGTAAAGCAATTAGCAGAGGCAGTGCAAAGAATATCCACAGAAAGCATAGTGAT
             3200
 TrpGlyArgThrProLysPheArgLeuProIleGlnLysGluThrTrpGluThrTrpTrp
ATGGGGAAGGACTCCTAAATTTAGACTACCCATACAAAAGGAAACATGGAAACATGGTG
                                                        3300
```

FIG.7D

```
AlaGluTyrTrpGlnAlaThrTrpIleProGluTrpGluPheValAsnThrProProLeu
GGCAGAGTATTGGCAAGCCACTTGGATTCCTGAGTGGGAATTTGTCAATACCCCTCCTTT

ValLysLeuTrpTyrGlnLeuGluLysGluProIleIleGlyAlaGluThrPheTyrVal
AGTAAAATTATGGTACCAGTTAGAGAAGGAACCCATAATAGGAGCAGAAACTTTCTATGT
                                        3400
AspGlyAlaAlaAsnArgGluThrLysLeuGlyLysAlaGlyTyrValThrAspArgGly
AGATGGGGCAGCTAATAGAGAGACTAAATTAGGAAAAGCAGGATATGTTACTGACAGAGG

ArgGlnLysValValProLeuThrAspThrThrAsnGlnLysThrGluLeuGlnAlaIle
AAGACAGAAAGTTGTCCCTTTGACTGACACGACAAATCAGAAGACTGAGTTACAAGCAAT
          3500
AsnLeuAlaLeuGlnAspSerGlyLeuGluValAsnIleValThrAspSerGlnTyrAla
TAATCTAGCCTTGCAGGATTCGGGATTAGAAGTAAACATAGTAACAGATTCACAATATGC
                                                        3600
LeuGlyIleIleGlnAlaGlnProAspLysSerGluSerGluLeuValAsnGlnIleIle
ATTAGGAATCATTCAAGCACAACCAGATAAGAGTGAATCAGAGTTAGTCAATCAAATAAT

GluGlnLeuIleLysLysGluLysValTyrLeuAlaTrpValProAlaHisLysGlyIle
AGAGCAGTTAATAAAAAAGGAAAAGGTTTACCTGGCATGGGTACCAGCACACAAAGGAAT
                                        3700
GlyGlyAsnGluGlnValAspLysLeuValSerGlnGlyIleArgLysValLeuPheLeu
TGGAGGAAATGAACAAGTAGATAAATTAGTCAGTCAAGGAATCAGGAAAGTACTATTTTT

AspGlyIleAspLysAlaGlnGluGluHisGluLysTyrHisAsnAsnTrpArgAlaMet
GGATGGAATAGATAAGGCTCAAGAAGAACATGAGAAATATCACAACAATTGGAGAGCAAT
          3800
AlaSerAspPheAsnLeuProProValValAlaLysGluIleValAlaSerCysAspLys
GGCTAGTGATTTTAACCTACCACCCGTGGTAGCAAAAGAAATAGTAGCTAGCTGTGATAA
                                                        3900
CysGlnLeuLysGlyGluAlaMetHisGlyGlnValAspCysSerProGlyIleTrpGln
ATGTCAGCTAAAAGGAGAAGCCATGCATGGACAAGTAGACTGTAGTCCAGGAATATGGCA

LeuAspCysThrHisLeuGluGlyLysValIleLeuValAlaValHisValAlaSerGly
ATTAGATTGTACACACTTAGAAGGAAAAGTTATCCTGGTAGCAGTTCATGTAGCCAGTGG
                                        4000
TyrIleGluAlaGluValIleProAlaGluThrGlyGlnGluThrAlaTyrPheLeuLeu
CTATATAGAAGCAGAAGTTATTCCAGCAGAAACAGGGCAGGAAACAGCATATTTTCTTTT

LysLeuAlaGlyArgTrpProValLysValValHisThrAspAsnGlySerAsnPheThr
AAAATTAGCAGGAAGATGGCCAGTAAAAGTAGTACATACAGACAATGGCAGCAATTTCAC
          4100
SerAlaAlaValLysAlaAlaCysTrpTrpAlaGlyIleLysGlnGluPheGlyIlePro
CAGTGCTGCAGTTAAGGCCGCCTGTTGGTGGGCAGGTATCAAACAGGAATTTGGAATTCC
                                                        4200
TyrAsnProGlnSerGlnGlyValValGluSerMetAsnLysGluLeuLysLysIleIle
CTACAATCCCCAAAGTCAAGGAGTAGTAGAATCTATGAATAAAGAATTAAAGAAAATTAT

GlyGlnValArgAspGlnAlaGluHisLeuLysThrAlaValGlnMetAlaValPheIle
AGGACAGGTAAGAGATCAAGCTGAACATCTTAAGACAGCAGTACAAATGGCAGTATTCAT
                                        4300
HisAsnPheLysArgArgArgGlyIleGlyGlyTyrSerAlaGlyGluArgIleIleAsp
CCACAATTTTAAAAGAAGAAGGGGGATTGGGGGATACAGTGCAGGGGAAAGAATAATAGA
```

FIG. 7E

```
 IleIleAlaThrAspIleGlnThrLysGluLeuGlnLysGlnIleIleLysIleGlnAsn
CATAATAGCAACAGACATACAAACTAAAGAATTACAAAAACAAATTATAAAAATTCAAAA
                4400
 PheArgValTyrTyrArgAspSerArgAspProIleTrpLysGlyProAlaLysLeuLeu
TTTTCGGGTTTATTACAGAGACAGCAGAGATCCAATTTGGAAAGGACCAGCAAAGCTCCT
                                                         4500
 TrpLysGlyGluGlyAlaValValIleGlnAspLysSerAspIleLysValValProArg
CTGGAAAGGTGAAGGGGCAGTAGTAATACAAGACAAGAGTGACATAAAGGTAGTACCAAG
                            Q
 ArgLysValLysIleIleArgAspTyrGlyLysGlnMetAlaGlyAspAspCysValAla
                         MetGluAsnArgTrpGlnValMetIleValTrpGln
AAGAAAAGTAAAGATTATTAGGATTATGGAAAACAGATGGCAGGTGATGATTGTGTGGC
             POL                        4600
 SerArgGlnAspGluAsp
  ValAspArgMetArgIleLysThrTrpLysSerLeuValLysHisHisMetTyrValSer
AAGTAGACAGGATGAGGATTAAAACATGGAAAAGTTTAGTAAAACACCATATGTATGTTT

  LysLysAlaAsnArgTrpPheTyrArgHisHisTyrGluSerProHisProLysIleSer
CAAAGAAAGCTAACAGATGGTTTTATAGACATCACTATGAAAGCCCCCACCCAAAAATAA
                4700
  SerGluValHisIleProLeuGlyGluAlaArgLeuValIleLysThrTyrTrpGlyLeu
GTTCAGAAGTACACATCCCACTAGGAGAAGCTAGACTGGTAATAAAAACATATTGGGGTC
                                                         4800
  HisThrGlyGluArgGluTrpHisLeuGlyGlnGlyValSerIleGluTrpArgLysArg
TGCATACAGGAGAAAGAGAATGGCATCTGGGTCAGGGAGTCTCCATAGAATGGAGGAAAA

  ArgTyrSerThrGlnValAspProGlyLeuAlaAspGlnLeuIleHisMetTyrTyrPhe
GGAGATATAGCACACAAGTAGACCCTGGCCTGGCAGACCAACTAATTCATATGTATTATT
                                        4900
  AspCysPheSerGluSerAlaIleArgLysAlaIleLeuGlyAspIleValSerProArg
TTGATTGTTTTTCAGAATCTGCTATAAGAAAAGCCATATTAGGAGATATAGTTAGTCCTA

  CysGluTyrGlnAlaGlyHisAsnLysValGlySerLeuGlnTyrLeuAlaLeuThrAla
GGTGTGAGTATCAAGCAGGACATAACAAGGTAGGATCCCTACAGTATTTGGCACTAACAG
                5000
  LeuIleAlaProLysGlnIleLysProProLeuProSerValArgLysLeuThrGluAsp
CATTAATAGCACCAAAACAGATAAAGCCACCTTTGCCTAGTGTTAGGAAGCTAACAGAAG
       R                                                 5100
    MetGluGlnAlaProAlaAspGlnGlyProGlnArgGluProTyrAsnGluTrpAla
  ArgTrpAsnLysProGlnGlnThrArgGlyHisArgGlySerHisThrMetAsnGlyHis
ATAGATGGAACAAGCCCCAGCAGACCAGGGGCCACAGAGGGAGCCATACAATGAATGGGC
Q
  LeuGluLeuLeuGluGluLeuLysSerGluAlaValArgHisPheProArgIleTrpLeu
ATTAGAGCTTTTAGAGGAGCTTAAGAGTGAAGCTGTTAGACATTTTCCTAGGATATGGCT
                                        5200
 HisSerLeuGlyGlnHisIleTyrGluThrTyrGlyAspThrTrpValGlyValGluAla
CCATAGCTTAGGACAACATATTTATGAAACTTATGGGGATACCTGGGTAGGAGTTGAAGC

 IleIleArgIleLeuGlnGlnLeuLeuPheIleHisPheArgIleGlyCysGlnHisSer
TATAATAAGAATACTGCAACAATTACTGTTTATTCATTTCAGAATTGGGTGTCAACATAG
                5300                   S          R
 ArgIleGlyIleIleArgGlnArgArgAlaArgAsnGlySerSerArgSer
                                    MetAspProValAspProAsnLeuGlu
CAGAATAGGCATTATTCGACAGAGAAGAGCAAGAAATGGATCCAGTAGATCCTAACCTAG
                                                         5400
```

FIG. 7F

```
ProTrpAsnHisProGlySerGlnProArgThrProCysAsnLysCysHisCysLysLys
AGCCCTGGAACCATCCAGGAAGTCAGCCTAGGACTCCTTGTAACAAGTGTCATTGTAAAA

CysCysTyrHisCysProValCysPheLeuAsnLysGlyLeuGlyIleSerTyrGlyArg
AGTGTTGCTATCATTGCCCAGTTTGCTTCTTAAACAAAGGCTTAGGCATCTCCTATGGCA
                                   5500
LysLysArgArgGlnArgArgGlyProProGlnGlyGlyGlnAlaHisGlnValProIle
GGAAGAAGCGGAGACAGCGACGAGGACCTCCTCAAGGCGGTCAGGCTCATCAAGTTCCTA
         S
ProLysGln
TACCAAAGCAGTAAGTAGTACATGTAATGCAACCTTTAGGGATAATAGCAATAGCAGCAT
           5600
TAGTAGTAGCAATAATACTAGCAATAGTTGTGTGGACCATAGTATTCATAGAATATAGAA
                                                        5700
GGATAAAAAAGCAAAGGAGAATAGACTGTTTACTTGATAGAATAACAGAAAGAGCAGAAG
         ENV
         MetArgAlaArgGlyIleGluArgAsnCysGlnAsnTrpTrpLysTrpGly
ACAGTGGCAATGAGAGCGAGGGGGATAGAGAGAAATTGTCAAAACTGGTGGAAATGGGGC
                                   5800
IleMetLeuLeuGlyIleLeuMetThrCysSerAlaAlaAspAsnLeuTrpValThrVal
ATCATGCTCCTTGGGATATTGATGACCTGTAGTGCTGCAGACAATCTGTGGGTCACAGTT

TyrTyrGlyValProValTrpLysGluAlaThrThrThrLeuPheCysAlaSerAspAla
TATTATGGGGTGCCTGTATGGAAGGAAGCAACCACCACTCTATTTTGTGCATCAGATGCT
           5900
LysSerTyrGluThrGluAlaHisAsnIleTrpAlaThrHisAlaCysValProThrAsp
AAATCATATGAAACAGAGGCACATAATATCTGGGCCACACATGCCTGTGTACCCACGGAC
                                                        6000
ProAsnProGlnGluIleAlaLeuGluAsnValThrGluAsnPheAsnMetTrpLysAsn
CCCAACCCACAAGAAATAGCACTGGAAAATGTGACAGAAAACTTTAACATGTGGAAAAAT

AsnMetValGluGlnMetHisGluAspIleIleSerLeuTrpAspGlnSerLeuLysPro
AACATGGTGGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAAAGCCTAAAACCA
                                   6100
CysValLysLeuThrProLeuCysValThrLeuAsnCysSerAspGluLeuArgAsnAsn
TGTGTAAAATTAACCCCACTCTGTGTCACTTTAAACTGTAGTGATGAATTGAGGAACAAT

GlyThrMetGlyAsnAsnValThrThrGluGluLysGlyMetLysAsnCysSerPheAsn
GGCACTATGGGGAACAATGTCACTACAGAGGAGAAAGGAATGAAAAACTGCTCTTTCAAT
           6200
ValThrThrValLeuLysAspLysLysGlnGlnValTyrAlaLeuPheTyrArgLeuAsp
GTAACCACAGTACTAAAAGATAAGAAGCAGCAAGTATATGCACTTTTTTATAGACTTGAT
                                                        6300
IleValProIleAspAsnAspSerSerThrAsnSerThrAsnTyrArgLeuIleAsnCys
ATAGTACCAATAGACAATGATAGTAGTACCAATAGTACCAATTATAGGTTAATAAATTGT

AsnThrSerAlaIleThrGlnAlaCysProLysValSerPheGluProIleProIleHis
AATACCTCAGCCATTACACAGGCTTGTCCAAAGGTATCCTTTGAGCCAATTCCCATACAT
                                   6400
TyrCysAlaProAlaGlyPheAlaIleLeuLysCysArgAspLysLysPheAsnGlyThr
TATTGTGCCCCAGCTGGTTTTGCGATTCTAAAGTGTAGAGATAAGAAGTTCAATGGAACA

GlyProCysThrAsnValSerThrValGlnCysThrHisGlyIleArgProValValSer
GGCCCATGCACAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAGTGGTGTCA
           6500
```

FIG. 7G

```
ThrGlnLeuLeuLeuAsnGlySerLeuAlaGluGluGluValIleIleArgSerGluAsn
ACTCAACTGCTGTTGAATGGCAGTCTAGCAGAAGAAGAGGTCATAATTAGATCCGAAAAT
                                                        6600
LeuThrAsnAsnAlaLysAsnIleIleAlaHisLeuAsnGluSerValLysIleThrCys
CTCACAAACAATGCTAAAAACATAATAGCACATCTTAATGAATCTGTAAAAATTACCTGT

AlaArgProTyrGlnAsnThrArgGlnArgThrProIleGlyLeuGlyGlnSerLeuTyr
GCAAGGCCCTATCAAAATACAAGACAAAGAACACCTATAGGACTAGGGCAATCACTCTAT
                                          6700
ThrThrArgSerArgSerIleIleGlyGlnAlaHisCysAsnIleSerArgAlaGlnTrp
ACTACAAGATCAAGATCAATAATAGGACAAGCACATTGTAATATTAGTAGAGCACAATGG

SerLysThrLeuGlnGlnValAlaArgLysLeuGlyThrLeuLeuAsnLysThrIleIle
AGTAAAACTTTACAACAAGTAGCTAGAAAATTAGGAACCCTTCTTAACAAAACAATAATA
               6800
LysPheLysProSerSerGlyGlyAspProGluIleThrThrHisSerPheAsnCysGly
AAGTTTAAACCATCCTCAGGAGGGGACCCAGAAATTACAACACACAGTTTTAATTGTGGA
                                                        6900
GlyGluPhePheTyrCysAsnThrSerGlyLeuPheAsnSerThrTrpAsnIleSerAla
GGGGAATTCTTCTACTGTAATACATCAGGACTGTTTAATAGTACATGGAATATTAGTGCA

TrpAsnAsnIleThrGluSerAsnAsnSerThrAsnThrAsnIleThrLeuGlnCysArg
TGGAATAATATTACAGAGTCAAATAATAGCACAAACACAAACATCACACTCCAATGCAGA
                                          7000
IleLysGlnIleIleLysMetValAlaGlyArgLysAlaIleTyrAlaProProIleGlu
ATAAAACAAATTATAAAGATGGTGGCAGGCAGGAAAGCAATATATGCCCCTCCTATCGAA

ArgAsnIleLeuCysSerSerAsnIleThrGlyLeuLeuLeuThrArgAspGlyGlyIle
AGAAACATTCTATGTTCATCAAATATTACAGGGCTACTATTGACAAGAGATGGTGGTATA
               7100
AsnAsnSerThrAsnGluThrPheArgProGlyGlyGlyAspMetArgAspAsnTrpArg
AATAATAGTACTAACGAGACCTTTAGACCTGGAGGAGGAGATATGAGGGACAATTGGAGA
                                                        7200
SerGluLeuTyrLysTyrLysValValGlnIleGluProLeuGlyValAlaProThrArg
AGTGAATTATATAAATATAAGGTAGTACAAATTGAACCACTAGGAGTAGCACCCACCAGG

AlaLysArgArgValValGluArgGluLysArgAlaIleGlyLeuGlyAlaMetPheLeu
GCAAAGAGAAGAGTGGTGGAAAGAGAAAAAAGAGCAATAGGATTAGGAGCTATGTTCCTT
                                          7300
GlyPheLeuGlyAlaAlaGlySerThrMetGlyAlaArgSerValThrLeuThrValGln
GGGTTCTTGGGAGCAGCAGGAAGCACGATGGGCGCACGGTCAGTGACGCTGACGGTACAG

AlaArgGlnLeuMetSerGlyIleValGlnGlnGlnAsnAsnLeuLeuArgAlaIleGlu
GCCAGACAATTAATGTCTGGTATAGTGCAACAGCAAAACAATTTGCTGAGGGCTATAGAG
               7400
AlaGlnGlnHisLeuLeuGlnLeuThrValTrpGlyIleLysGlnLeuGlnAlaArgIle
GCGCAACAGCATCTGTTGCAACTCACGGTCTGGGGCATTAAACAGCTCCAGGCAAGAATC
                                                        7500
LeuAlaValGluArgTyrLeuLysAspGlnGlnLeuLeuGlyIleTrpGlyCysSerGly
CTGGCTGTGGAAAGATACCTAAAGGATCAACAGCTCCTAGGAATTTGGGGTTGCTCTGGA
```

FIG. 7H

```
LysHisIleCysThrThrAsnValProTrpAsnSerSerTrpSerAsnArgSerLeuAsn
AAACACATTTGCACCACTAATGTGCCCTGGAACTCTAGTTGGAGTAATAGATCTCTAAAT
          .         .         .       7600         .         .
GluIleTrpGlnAsnMetThrTrpMetGluTrpGluArgGluIleAspAsnTyrThrGly
GAGATTTGGCAGAACATGACCTGGATGGAGTGGGAAAGAGAAATTGACAATTACACAGGC
          .         .         .         .         .         .
LeuIleTyrSerLeuIleGluGluSerGlnThrGlnGlnGluLysAsnGluLysGluLeu
TTAATATATAGCTTAATTGAGGAATCGCAGACCCAGCAAGAAAAGAATGAAAAAGAATTG
          .    7700           .         .         .         .
LeuGluLeuAspLysTrpAlaSerLeuTrpAsnTrpPheSerIleThrGlnTrpLeuTrp
TTGGAATTGGACAAGTGGGCAAGTTTGTGGAATTGGTTTAGCATAACACAATGGCTGTGG
          .         .         .         .         .      7800
TyrIleLysIlePheIleMetIleIleGlyGlyLeuIleGlyLeuArgIleValPheAla
TATATAAAAATATTCATAATGATAATAGGAGGCTTGATAGGTTTAAGAATAGTTTTTGCT
          .         .         .         .         .         .
ValLeuSerLeuValAsnArgValArgGlnGlyTyrSerProLeuSerPheGlnThrLeu
GTGCTTTCTTTAGTAAATAGAGTTAGGCAGGGATACTCACCTCTGTCGTTTCAGACCCTC
          .         .         .       7900         .         .
LeuProAlaProArgGlyProAspArgProGluGlyThrGluGluGluGlyGlyGluArg
CTCCCAGCCCCGAGGGGACCCGACAGGCCCGAAGGAACAGAAGAAGAAGGTGGAGAGCGA
          .         .         .         .         .         .
GlyArgAspArgSerValArgLeuLeuAsnGlyPheSerAlaLeuIleTrpAspAspLeu
GGCAGAGACAGATCCGTGAGATTGCTGAACGGATTCTCGGCACTTATCTGGGACGACCTG
          .    8000           .         .         .         .
ArgSerLeuCysLeuPheSerTyrHisArgLeuArgAspLeuIleLeuIleAlaValArg
CGGAGCCTGTGCCTCTTCAGCTACCACCGCTTGAGAGACTTAATCTTAATTGCAGTGAGG
          .         .         .         .         .      8100
IleValGluLeuLeuGlyArgArgGlyTrpAspIleLeuLysTyrLeuTrpAsnLeuLeu
ATTGTAGAACTTCTGGGACGCAGGGGGTGGGACATCCTCAAATATCTGTGGAATCTCCTA
          .         .         .         .         .         .
GlnTyrTrpSerGlnGluLeuArgAsnSerAlaSerSerLeuPheAspAlaIleAlaIle
CAGTATTGGAGTCAGGAACTGAGGAACAGTGCTAGTAGCTTGTTTGATGCCATAGCAATA
          .         .         .       8200         .         .
AlaValAlaGluGlyThrAspArgValIleGluIleIleGlnArgAlaCysArgAlaVal
GCAGTAGCTGAGGGGACAGATAGAGTTATAGAAATAATACAAAGAGCTTGCAGAGCTGTT
          .         .         .         .    W <-┐    .         .
LeuAsnIleProArgArgIleArgGlnGlyLeuGluArgSerLeuLeu         ┌->F
                                                         MetGlyGly
CTTAACATACCCAGAAGAATAAGACAGGGCTTAGAAAGGTCTTTACTTTAAAATGGGTGG.
          .    8300           .         .         .         .
 LysTrpSerLysSerSerIleValGlyTrpProAlaIleArgGluArgIleArgArgThr
CAAATGGTCAAAAAGTAGTATAGTGGGATGGCCTGCTATAAGGGAAAGAATAAGAAGAAC
          .         .         .         .         .      8400
 AsnProAlaAlaAspGlyValGlyAlaValSerArgAspLeuGluLysHisGlyAlaIle
TAATCCAGCAGCAGATGGGGTAGGAGCAGTATCTCGAGACCTGGAAAAACATGGGGCAAT
          .         .         .         .         .         .
 ThrSerSerAsnThrAlaSerThrAsnAlaAspCysAlaTrpLeuGluAlaGlnGluGlu
CACAAGTAGCAATACAGCAAGTACTAATGCTGACTGTGCCTGGCTAGAAGCACAAGAAGA
          .         .         .       8500         .         .
 SerAspGluValGlyPheProValArgProGlnValProLeuArgProMetThrTyrLys
GAGCGACGAGGTGGGCTTTCCAGTCAGACCCCAGGTACCTTTAAGACCAATGACTTACAA
          .         .         .         .  ┌-> U3   .         .
 GluAlaLeuAspLeuSerHisPheLeuLysGluLysGlyGlyLeuGluGlyLeuIleTrp
AGAAGCTCTAGATCTCAGCCACTTTTTAAAAGAAAAGGGGGGACTGGAAGGGCTAATTTG
          .    8600           .         .         .         .
```

FIG. 7I

```
 SerLysLysArgGlnGluIleLeuAspLeuTrpValTyrAsnThrGlnGlyIlePhePro
GTCCAAAAAGAGACAAGAGATCCTTGATCTTTGGGTCTACAACACACAAGGCATCTTCCC
          .         .         .         .         .     8700
 AspTrpGlnAsnTyrThrProGlyProGlyIleArgTyrProLeuThrPheGlyTrpCys
TGATTGGCAAAACTACACACCAGGGCCAGGGATCAGATATCCACTAACCTTTGGATGGTG
          .         .         .         .         .         .
 TyrGluLeuValProValAspProGlnGluValGluGluAspThrGluGlyGluThrAsn
CTACGAGCTAGTACCAGTTGATCCACAGGAGGTAGAAGAAGACACTGAAGGAGAGACCAA
          .         .         .        8800       .         .
 SerLeuLeuHisProIleCysGlnHisGlyMetGluAspProGluArgGlnValLeuLys
CAGCTTGTTACACCCTATATGCCAGCATGGAATGGAGGACCCGGAGAGACAAGTGTTAAA
          .         .         .         .         .         .
 TrpArgPheAsnSerArgLeuAlaPheGluHisLysAlaArgGluMetHisProGluPhe
ATGGAGATTTAACAGCAGACTAGCATTTGAGCACAAGGCCCGAGAGATGCATCCGGAGTT
          .     8900          .         .         .         .
 TyrLysAsn
CTACAAAAACTGATGACACCGAGCTTTCTACAAGGGACTTTCCGCTGGGGACTTTCCAGG
          .         .         .         .         .     9000
GAGGCGTGGACTGGGCGGGACTGGGGAGTGGCTAACCCTCAGATGCTGCATATAAGCAGC
          .    U3    R        .         .         .         .
TGCTTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATTTGAGCCTGGGAGCTCTCTC
          .         .         .        9100       .    B    .
GCTAGCTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTTGAGTGCTTCAA
          .         .         .         .         .
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